

Sujet de stage de Master recherche/Grandes écoles en informatique, mathématiques, biologie situé soit à Inria Paris-Rocquencourt EPI Contraintes, encadrant François Fages, soit à Université de Montpellier I, encadrant Ovidiu Radulescu.

Titre : Réduction de modèles à plusieurs échelles de temps en tant que réécriture de graphe.

Résumé : On se propose de formaliser un ensemble cohérent de règles de ré-écriture pour des modèles du type réseaux de réactions biochimiques. Ces règles, prenant en compte la nature multi-échelle de la dynamique permettront la réduction automatique de grands réseaux en biologie de systèmes. L'algorithme résultant sera implémenté dans un outil informatique.

Mots clés : abstraction, programmation par contraintes, biologie des systèmes

Title : Model reduction for multiscale biochemical networks by graph rewriting

Summary : We will formalise a coherent set of graph rewriting rules allowing to reduce networks of biochemical reactions. These rules are derived from classical approaches for model reduction in chemical kinetics (quasi-steady state, QSSA, quasi-equilibrium, QE approximations, lumping, averaging, finding a limiting rate reaction step) and consists in species and reactions pooling. The pools of reactions and species correspond to convex bases of the left and right kernels of the stoichiometric matrices of a fast subsystem. The computation of these convex bases (elementary modes) is NP hard but can be efficiently computed in practice as a constraint satisfaction problem.

The resulting reduction algorithms will be implemented in a computational biology tool.

Keywords : abstraction, constraint programming, systems biology

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